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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/020,139	12/18/2001	Roxanne Duan	PF348C1	7037

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EXAMINER
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ART UNIT	PAPER NUMBER
1644	8

DATE MAILED: 10/22/2002

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No. 10/020,139	Applicant(s) DUAN ET AL.	
	Examiner Michail A Belyavskyi	Art Unit 1644	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *18 December 2001 and 15 July 2002* .

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-15,17-34 and 36* is/are pending in the application.

4a) Of the above claim(s) *15 and 17* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-14,18-34 and 36* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *18 December 2001* is/are: a)☐ accepted or b)☒ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

11)☐ The proposed drawing correction filed on _____ is: a)☐ approved b)☐ disapproved by the Examiner.

If approved, corrected drawings are required in reply to this Office action.

12)☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. §§ 119 and 120

13)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____ .

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

14)☒ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).

a)☐ The translation of the foreign language provisional application has been received.

15)☒ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449) Paper No(s) _____ .
4) ☐ Interview Summary (PTO-413) Paper No(s). _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other:

DETAILED ACTION

1. Claims 1-15, 17-34 and 36 are pending.

2. Applicant's election with traverse of Group I, Claims 1-14, 18-34 and 36 in Paper No. 7 is acknowledged. Applicant traverse the Restriction Requirement on the grounds that the search of Groups I-III together would not constitute a serious search burden on the examiner and that search of the claims of Group I would provide useful information for the claims of Group II and Group III. This is not found persuasive because the MPEP 803 (August 2001) states that "For purposes of the initial requirement, a serious burden on the examiner may be prima facie shown if the examiner shows by appropriate explanation either separate classification, separate status in the art, or a different field of search". The Restriction Requirement enunciated in the previous Office Action meets this criterion and therefore establishes that serious burden is placed on the examiner by the examination Groups. The Inventions are distinct for reasons elaborated in paragraphs 3-6 of the previous Office Action, Paper NO:6.

The requirement is still deemed proper and is therefore made FINAL.

Claims 15 and 17 are withdrawn from further consideration by the Examiner, 37 C.F.R. § 1.142(b) as being drawn to nonelected inventions.

Claims 1-14, 18-34 and 36 are under consideration in the instant application.

3. The first sentence of the specification should be amended to reflect the status of the parent application 08/993,529.

4. The title of the invention is not descriptive. A new title is required that is clearly indicative of the invention *to which the claims are directed*

5. Formal drawings have been submitted which fail to comply with 37 CFR 1.84. Please see the enclosed form PTO-948.

INFORMATION ON HOW TO EFFECT DRAWING CHANGES

A. Correction of Informalities -- 37 CFR 1.85

New corrected drawings must be filed with the changes incorporated therein. Identifying indicia, if provided, should include the title of the invention, inventor's name, and application number, or docket number (if any) if an application number has not been assigned to the application. If this information is provided, it must be placed on the front of each sheet and centered within the top margin. If corrected drawings are required in a Notice of Allowability (PTOL-37), the new drawings **MUST** be filed within the **THREE MONTH** shortened statutory period set for reply in the "Notice of Allowability." Extensions of time may NOT be obtained under the provisions of 37 CFR 1.136 for filing the corrected drawings after the mailing of a Notice of Allowability. The drawings should be filed as a separate paper with a transmittal letter addressed to the Official Draftsperson.

B. Corrections other than Informalities Noted by Draftsperson on form PTO-948.

All changes to the drawings, other than informalities noted by the Draftsperson, **MUST** be made in the same manner as above except that, normally, a highlighted (preferably red ink) sketch of the changes to be incorporated into the new drawings **MUST** be approved by the examiner before the application will be allowed. No changes will be permitted to be made, other than correction of informalities, unless the examiner has approved the proposed changes.

Timing of Corrections

Applicant is required to submit acceptable corrected drawings within the time period set in the Office action. See 37 CFR 1.185(a). Failure to take corrective action within the set (or extended) period will result in ABANDONMENT of the application.

6. 35 U.S.C. § 101 reads as follows:

"Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter or any new and useful improvement thereof, may obtain a patent therefore, subject to the conditions and requirements of this title".

7. Claims 1-14, 18-34 and 36 are rejected under 35 U.S.C. 101 as the claimed invention is not supported by either a specific and substantial asserted utility or a well-established utility.

Applicant is directed to the Revised Interim Utility Guidelines, Federal Register, Vol. 64, No. 244, pages 71427-71440, Tuesday December 21, 1999. In keeping with the revised utility guidelines and corresponding training materials (available on the PTO Website), none of the disclosed uses is a specific, credible and/or substantial use.

The specification disclosed a nucleic acid molecules comprising a polynucleotide encoding at least a portion of the human Parotid Secretory Protein (hPSP) having the complete amino acid sequence of SEQ ID: 2 or the complete amino acid sequence encoded by the cDNA clone deposited in bacterial host as ATCC Deposit NO 97811 and nucleotide sequence (SEQ ID NO:1) determined by sequencing the deposited hPSP clone (pages 5-6 of the specification as filed). The specification fails to provide sufficient objective evidence of any activity for encoded proteins, or to show that these proteins even exist. Applicant only states that the sequence has homology to murine PSP (page 6, lines 10-12 of the specification as filed). No well-established utility for a human PSP family member is indicated. A well-established utility is a specific, substantial, and credible utility that is well known, immediately apparent, or implied by the specification's disclosure of the properties of a material.

Identifying a polynucleotide as encoding a murine-PSP-like protein does not endow the polynucleotide with such a utility. The instant specification discloses the immunolocalization of the PSP family of proteins primarily to the parotid gland in mouse (pages 2-3 of the specification, as filed), but the physiological role of the PSP family has not been clarified. The only distinguishing characteristics disclosed of the family are similarity in the signal peptide and the presence of two cysteine residues spaced a uniform distance apart from one another in all family members (page 4, lines 27-36 for example), but no functional correlation for this feature is disclosed. Identifying a protein as having a limited homology to this protein, which is not known to be a member of a family of similarly-acting factors with identifiable functional regions, does not indicate what function it and thus the encoding polynucleotide might have.

In support, Skolnick et al. (Trends in Biotech., 18(1):34-39, 2000) disclose that the skilled artisan is well aware that assigning functional activities for any particular protein or protein family based upon sequence homology is inaccurate, in part because of the multifunctional nature of proteins (e.g., "Abstract" and "Sequence-based approaches to function prediction", page 34). Even in situations where there is some confidence of a similar overall structure between two proteins, only experimental research can confirm the artisan's best guess as to the function of the structurally related protein (see in particular "Abstract" and Box 2). Thus, the homology-based assignment of human PSP as a parotid secretory protein does not appear to provide credible evidence of a specific and substantial utility based on the knowledge of the skilled artisan and the data presented in the instant specification. Attwood *et al.* (Science, 2000, 290, 471-473) teach that protein function is context-dependent and the state of the art of making functional assignments merely on the basis of some degree of similarity between sequences and the current structure prediction methods is unreliable.

There is no specific disease or specific function that is suggested by this limited homology. There is therefore no specific, substantial, or credible utility that is well-known, apparent, or implied by the relationship of the instant polynucleotide to the polynucleotide encoding murine PSP.

The claimed polynucleotides also lack a specific or substantial utility. The specification does not indicate that the sequences are full-length open reading frames. No evidence that the sequences are in frame and that the protein is actually produced is presented. The sequences could therefore be fragments. DNA fragments have no specific or substantial utility; their use to identify full-length sequences is a research use only.

The utilities identified by the applicant beginning on page 32 are also not specific or substantial. A utility such as chromosome localization would apply to virtually every naturally occurring polynucleotide and is therefore not specific. Likewise, tissue-specific expression does not rely on specific properties or functions of the encoded protein. Each nucleic acid sequence that is expressed within a multicellular organism is expressed in some cell type and this expression is regulated in either a temporal or spatial manner. That, is, each expressed sequence is expressed in some cell type at some point in a hosts lifetime. Some transcripts are expressed embryonically, others are expressed only in particular cells, while still others are expressed in a wide variety of cells. In addition, some transcripts which are expressed in particular cells are only expressed in response to certain metabolic or environmental stimuli. Therefore, mere expression does not appear to provide credible evidence of a specific and substantial utility based on the knowledge of the skilled artisan and the data presented in the instant specification.

Further, the specification does not disclose any diseases or conditions known to be associated with the encoded protein. Therefore, identification of mutations in the encoding gene would not be sufficient to identify or confirm a "real world" context of use; clearly further research would be required to identify a disease in which the encoded protein is involved and for which any mutations would be of significance; the polynucleotide therefore lacks a substantial utility.

Thus, the disclosed utilities do not appear to be either specific or substantial because the specification fails to disclose a specific and substantial credible utility for either the nucleic acid of SEQ ID NO:I or the polypeptide having the amino acid sequence of SEQ ID NO:2. Therefore, (1) An isolated nucleic acid molecule, comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group recited in claim 1, or complete nucleotide sequence of SEQ ID NO:1 (claim 2), or nucleotide sequence in SEQ ID NO:1 encoding the hPSP polypeptide having the amino acid sequence in position –17 to +231 of SEQ ID NO:2 (claim 3), or nucleotide sequence in SEQ ID NO:1 encoding the mature form of the hPSP polypeptide having the amino acid sequence from about amino acid residue 1 to about amino acid residue 231 of SEQ ID NO:2 (claim 4); or complete nucleotide sequence of the cDNA clone contained in ATCC Deposit No 97811(claim 6), or nucleotide sequence encoding the hPSP polypeptide having the complete amino acid sequence except the N-terminal amino acid encoded by the cDNA clone contained in ATCC Deposit No 97811 (claim 7) or nucleotide sequence encoding the mature form of the hPSP (claim 8); (2) an isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95 % identical to a sequence selected from the group recited in claim 5; (3) an isolated nucleic acid molecule comprising a nucleic acid sequence which encodes an epitope-bearing portion of an hPSP polypeptide selected from the group recited in claim 9; (4) a method of making recombinant vector , (claims 10 and 31) recombinant vector (claims 11 and 31), a method of making a recombinant host cell (claim 12) and a recombinant host cell (claims 13 and 33) and a method for producing a hPSP (claims 14 and 34); (5) an isolated nucleic acid molecule comprising a polynucleotide having a sequence

at least 95 % identical to a sequence selected from the group recited in claim 18; (6) an isolated polynucleotide comprising a nucleic acid sequence selected from the group recited in Claim 19, or comprising SEQ ID NO:1 (claim 22) or encoding a mature polypeptide (claim 24) or identical to the human cDNA contained in ATCC Deposit No. 97811 (claim 25) or encoding at least 50 contiguous amino acids of SEQ ID NO:2 (claim 27) or complementary to the polynucleotide of claim 19 (claim 28) ; (8) the isolated polynucleotide of claim 19, further comprising a hetorologus polynucleotide (claim 29), wherein said heterologous polynucleotide encodes a heterologous polypeptide (claim 30); (9) a composition comprising the isolated polynucleotide of claim 19 (claim 36) each appear to constitute research reagents for further experimentation to discover a "real world " utility for the claimed invention.

Thus, for the above mentioned reasons there does not appear to be either a specific and substantial credible asserted utility, or a well-established utility for the claimed : (1) An isolated nucleic acid molecule, comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group recited in claim 1, or complete nucleotide sequence of SEQ ID NO:1 (claim 2), or nucleotide sequence in SEQ ID NO:1 encoding the hPSP polypeptide having the amino acid sequence in position –17 to +231 of SEQ ID NO:2 (claim 3), or nucleotide sequence in SEQ ID NO:1 encoding the mature form of the hPSP polypeptide having the amino acid sequence from about amino acid residue 1 to about amino acid residue 231 of SEQ ID NO:2 (claim 4); or complete nucleotide sequence of the cDNA clone contained in ATCC Deposit No 97811(claim 6), or nucleotide sequence encoding the hPSP polypeptide having the complete amino acid sequence except the N-terminal amino acid encoded by the cDNA clone contained in ATCC Deposit No 97811 (claim 7) or nucleotide sequence encoding the mature form of the hPSP (claim 8); (2) an isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95 % identical to a sequence selected from the group recited in claim 5; (3) an isolated nucleic acid molecule comprising a nucleic acid sequence which encodes an epitope-bearing portion of an hPSP polypeptide selected from the group recited in claim 9; (4) a method of making recombinant vector , (claims 10 and 31) recombinant vector (claims 11 and 31), a method of making a recombinant host cell (claim 12) and a recombinant host cell (claims 13 and 33) and a method for producing a hPSP (claims 14 and 34); (5) an isolated nucleic acid molecule comprising a polynucleotide having a sequence at least 95 % identical to a sequence selected from the group recited in claim 18; (6) an isolated polynucleotide comprising a nucleic acid sequence selected from the group recited in Claim 19, or comprising SEQ ID NO:1 (claim 22) or encoding a mature polypeptide (claim 24) or identical to the human cDNA contained in ATCC Deposit No. 97811 (claim 25) or encoding at least 50 contiguous amino acids of SEQ ID NO:2 (claim 27) or complementary to the polynucleotide of claim 19 (claim 28) ; (8) the isolated polynucleotide of claim 19, further comprising a hetorologus polynucleotide (claim 29), wherein said heterologous polynucleotide encodes a heterologous polypeptide (claim 30); (9) a composition comprising the isolated polynucleotide of claim 19 (claim 36).

In addition, since SEQ ID NO:I itself appears to constitute a research reagent, vectors and host cells comprising SEQ ID NO:I or related sequences also do not appear to have a specific and substantial credible utility, or a well established utility.

Applicant is directed to the Utility Examination Guidelines, Federal Register, Vol. 66, No. 4, pages 1092-1099, Friday January 5, 2001.

As such, further research would be required. See Brenner v. Manson, 383 U.S. 519, 535-36, 148 USPQ 689, 696 (1966), the court indicates "a patent is not a hunting license. It is not a reward for the search, but compensation for its successful conclusion." A patent is therefore not a license to experiment. Because the claimed invention is not supported by a specific asserted utility for the reasons set forth, credibility of any utility cannot be assessed.

8. The following is a quotation of the first paragraph of 35 U.S.C. 112:
The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

9. Claims 1-14, 18-34 and 36 also rejected under 35 U.S.C. 112, first paragraph. Specifically, since the claimed invention is not supported by either a specific and substantial, credible asserted utility or a well established utility for the reasons set forth in the rejection under 35 USC101 above, one skilled in the art clearly would not know how to use the claimed invention.

10. Claims 1-14, 18-34 and 36 rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

A) While it is noted that Applicant has indicated that human hPSP cDNA clone was deposited with the ATCC , Deposit No:97811, the following requirements must still be met in order to fulfill the requirements of 37 CFR 1.801-1.809. (See also MPEP 2402-2411.)

If the deposits have been made under the terms of the Budapest Treaty, an affidavit or declaration by applicants or someone associated with the patent owner who is in a position to make such assurances, or a statement by an attorney of record over his or her signature, stating that the **cDNA clone** have been deposited under the Budapest Treaty and that the **cDNA clone** will be irrevocably and without restriction or condition released to the public upon the issuance of a patent would satisfy the deposit requirement made herein. See 37 CFR 1.808. Further, the record must be clear that the deposit will be maintained in a public depository for a period of 30 years after the date of deposit, 5 years after the last request for a sample, or for the enforceable life of the patent whichever is longer. See 37 CFR 1.806.

If the deposit has not been made under the Budapest treaty, then an affidavit or declaration by applicants or someone with the patent owner who is in a position to make such assurances, or a statement by an attorney of record over his or her signature must be made, stating that the deposit has been made at an acceptable depository and that the criteria set forth in 37 CFR 1.801-1.809, have been met.

B). The specification does not provide a sufficient enabling description of the claimed invention. The specification discloses only specific nucleic acid molecules comprising a polynucleotide encoding at least a portion of the human Parotid Secretory Protein (hPSP) having the complete amino acid sequence of SEQ ID: 2 or the complete amino acid sequence encoded by the cDNA clone deposited in bacterial host as ATCC Deposit NO 97811 and nucleotide sequence (SEQ ID NO:1) determined by sequencing the deposited hPSP clone (pages 5-6 of the specification as filed). The instant claims encompass in their breadth : (1) *Any* isolated nucleic acid molecule, comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group recited in claim 1, or complete nucleotide sequence of SEQ ID NO:1 (claim 2), or nucleotide sequence in SEQ ID NO:1 encoding the hPSP polypeptide having the amino acid sequence in position –17 to +231 of SEQ ID NO:2 (claim 3), or nucleotide sequence in SEQ ID NO:1 encoding the mature form of the hPSP polypeptide having the amino acid sequence from about amino acid residue 1 to about amino acid residue 231 of SEQ ID NO:2 (claim 4); or complete nucleotide sequence of the cDNA clone contained in ATCC Deposit No 97811(claim 6), or nucleotide sequence encoding the hPSP polypeptide having the complete amino acid sequence except the N-terminal amino acid encoded by the cDNA clone contained in ATCC Deposit No 97811 (claim 7) or nucleotide sequence encoding the mature form of the hPSP (claim 8); (2) *any* isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95 % identical to a sequence selected from the group recited in claim 5; (3) an isolated nucleic acid molecule comprising a nucleic acid sequence which encodes an epitope-bearing portion of an hPSP polypeptide selected from the group recited in claim 9; (4) a method of making *any* recombinant vector , (claims 10 and 31), *any* recombinant vector (claims 11 and 31), a method of making *any* recombinant host cell (claim 12) and a recombinant host cell (claims 13 and 33) and a method for producing a hPSP (claims 14 and 34); (5) *any* isolated nucleic acid molecule comprising a polynucleotide having a sequence at least 95 % identical to a sequence selected from the group recited in claim 18; (6) *any* isolated polynucleotide comprising a nucleic acid sequence selected from the group recited in Claim 19, or comprising SEQ ID NO:1 (claim 22) or encoding a mature polypeptide (claim 24) or identical to the human cDNA contained in ATCC Deposit No. 97811 (claim 25) or encoding at least 50 contiguous amino acids of SEQ ID NO:2 (claim 27) or complementary to the polynucleotide of claim 19 (claim 28) ; (8) *any* isolated polynucleotide of claim 19, further comprising a hetorologus polynucleotide (claim 29), wherein said heterologous polynucleotide encodes a heterologous polypeptide (claim 30); (9) a composition comprising *any* isolated polynucleotide of claim 19 (claim 36).

The specification fails to provide guidance as how to make (1) *Any* isolated nucleic acid molecule, comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group recited in claim 1, or complete nucleotide sequence of SEQ ID NO:1 (claim 2), or nucleotide sequence in SEQ ID NO:1 encoding the hPSP polypeptide having the amino acid sequence in position –17 to +231 of SEQ ID NO:2 (claim 3), or nucleotide sequence in SEQ ID NO:1 encoding the mature form of the hPSP polypeptide having the amino acid sequence from about amino acid residue 1 to about amino acid residue 231 of SEQ ID NO:2 (claim 4); or complete nucleotide sequence of the cDNA clone contained in ATCC Deposit No 97811(claim 6), or nucleotide sequence encoding the hPSP polypeptide having the complete amino acid sequence except the N-terminal amino acid encoded by the cDNA clone contained in ATCC Deposit No 97811 (claim 7) or nucleotide sequence encoding the mature form of the hPSP (claim 8); (2) *any* isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95 % identical to a sequence selected from the group recited in claim 5; (3) an isolated nucleic acid molecule comprising a nucleic acid sequence which encodes an epitope-bearing portion of an hPSP polypeptide selected from the group recited in claim 9; (4) a method of making *any* recombinant vector , (claims 10 and 31), *any* recombinant vector (claims 11 and 31), a method of making *any* recombinant host cell (claim 12) and a recombinant host cell (claims 13 and 33) and a method for producing a hPSP (claims 14 and 34); (5) *any* isolated nucleic acid molecule comprising a polynucleotide having a sequence at least 95 % identical to a sequence selected from the group recited in claim 18; (6) *any* isolated polynucleotide comprising a nucleic acid sequence selected from the group recited in Claim 19, or comprising SEQ ID NO:1 (claim 22) or encoding a mature polypeptide (claim 24) or identical to the human cDNA contained in ATCC Deposit No. 97811 (claim 25) or encoding at least 50 contiguous amino acids of SEQ ID NO:2 (claim 27) or complementary to the polynucleotide of claim 19 (claim 28) ; (8) *any* isolated polynucleotide of claim 19, further comprising a hetorologus polynucleotide (claim 29), wherein said heterologous polynucleotide encodes a heterologous polypeptide (claim 30); (9) a composition comprising *any* isolated polynucleotide of claim 19 (claim 36) without undue experimentation.

There does not appear to be sufficient guidance in the specification as filed as to how the skilled artisan would make the various nucleic acids recited in the instant claims. A person of skill in the art would not know which sequences are essential and which sequences are non-essential. There is insufficient guidance to direct a person of skill in the art to select particular sequences or sequence lengths as essential for the function of nucleic acid sequence of SEQ ID NO:I and polypeptide encoded by the amino acid sequence of SEQ ID NO: II. Moreover, there is insufficient guidance as to which "isolated polynucleotide comprising a heterologous polynucleotide", recited in the claim 29 and which "heterologous polypeptide" recited in claim 30, would maintain the same function as polypeptide encoded by amino acid sequence of SEQ ID NO: II.

Thus there appears to be insufficient guidance in the specification as filed to direct a person skill in the art to *select particular nucleotide sequence as encoding amino acids essential for the*

functional properties of the polypeptide. In addition, no functional properties of hPSP even disclosed.

Since the nucleic acid sequence of a polynucleotide determines its protein coding properties, predictability of which changes can be tolerated in a polynucleotide's nucleic acid sequence and still retain similar functions and properties requires a knowledge of, and guidance with regard to which nucleic acids within the full-length nucleotide sequence, if any, are tolerant of modification and which are conserved or less tolerant to modification, and detailed knowledge of the ways in which the product's structure relates to its functional usefulness. Because there is no guidance in the specification as to which amino acids sequence within the full-length amino acid sequence of SEQ ID NO: 2, which encoded hPSP that after substitution, deletion or insertion will retain the same function, it is unpredictable to determine which polynucleotide comprising a polynucleotide sequence that encodes a polynucleotide sequence that has at least "95% identity" to the nucleic acid sequence, encoding the hPSP of SEQ ID NO: 2 will have similar function. Since the structure associated with functions of any polynucleotide mentioned above are not disclosed, predicting which polynucleotide that has at least 95% identity to the nucleic acid sequence , encoding the hPSP of SEQ ID NO: 2 having the same function as amino acid sequence of SEQ ID NO: 2 is well outside the realm of routine experimentation.

The instant Claims encompass fragments. For example, claim 18 recite a nucleic acid comprising of a fragment of at least 30 contiguous nucleotides from 48 to 793 nucleotides of nucleotide sequence of SEQ ID NO: 1 or a complement thereof ,claim 19 recite a nucleic acid sequence encoding a polypeptide of at least 30 contiguous amino acid of SEQ ID NO:2 and claim 27 recite a nucleic acid sequence encoding a polypeptide of at least 50 contiguous amino acids of SEQ ID NO:2. There is insufficient guidance as to which nucleic acid residue within the nucleic acid sequence mention above or amino acid sequence within a polypeptide encoded by amino acid sequence of SEQ ID NO: 2 are *essential for the functional properties of nucleic acid molecule or the encoded polypeptide.*

As discussed supra, Skolnick et al. (Trends in Biotech., 18(1):34-39, 2000) teach that the skilled artisan is well aware that assigning functional activities for any particular protein or protein family based upon sequence homology is inaccurate, in part because of the multifunctional nature of proteins (e.g., "Abstract" and "Sequence-based approaches to function prediction", page 34). Even in situations where there is some confidence of a similar overall structure between two proteins, only experimental research can confirm the artisan's best guess as to the function of the structurally related protein (see in particular "Abstract" and Box 2).

Ngo *et al* teach that the amino acid positions within the polypeptide/protein that can tolerate change such as conservative substitution or no substitution, addition or deletion which are critical to maintain the protein's structure will require guidance (see Ngo *et al.*, 1994, The protein Folding Problem and Tertiary Structure Prediction, pp.492-495). Similarly, Skolnick *et al.* (Trends in Biotech., 18(1):34-39, 2000) teach that sequence-based methods for function prediction are inadequate because of the multifunctional nature of proteins (see the abstract Page 34). Such a recitation does not require that the nucleic acid encode the full length sequence set forth in SEQ ID NO:I; but rather encompasses any nucleic acid sequence comprising either the full length of SEQ ID NO:I or any contiguous nucleic acid residues. Without sufficient guidance, the changes which can be made in nucleic acid sequence of SEQ ID NO: I and still maintain activity is unpredictable and the experimentation left to those skilled in the art is unnecessarily, and improperly, extensive and undue.

In re Fisher, 1666 USPQ 19 24 (CCPA 1970) indicates that the more unpredictable an area is, the more specific enablement is necessary in order to satisfy the statute.

Reasonable correlation must exist between the scope of the claim and the scope of enablement set forth. Without sufficient guidance, the changes which can be made in the instantly recited nucleic acid sequences or proteins encoded by the recited nucleic acid sequences and still maintained the functional properties of SEQ ID NO: I and protein encoded by SEQ ID NO: 2 is unpredictable, as is the identity of which fragments would encode a functional polypeptide since the amino acids encoding a particular functional activity do not appear to have been identified; thus the experimentation left to those skilled in the art is unnecessary, improperly, extensive and undue.

In view of the quantity of experimentation necessary, absence of working examples, the unpredictability of the art, the lack of sufficient guidance in the specification, and the breadth of the claims, it would take undue trials and errors to practice the claimed invention.

11. Claims 1-14,18-20, 26-34 and 36 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Applicant is in possession of a complete amino acid sequence of SEQ ID: 2 or the complete amino acid sequence encoded by the cDNA clone deposited in bacterial host as ATCC Deposit NO 97811 and nucleotide sequence of SEQ ID NO:1 and a method of producing a hPSP polypeptide, encoded by amino acid sequence of SEQ ID NO:2.

Applicant in not in possession of: (1) *Any* isolated nucleic acid molecule, comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group recited in claim 1, or complete nucleotide sequence of SEQ ID NO:1 (claim 2), or nucleotide sequence in SEQ ID NO:1 encoding the hPSP polypeptide having the amino acid sequence in position –17 to +231 of SEQ ID NO:2 (claim 3), or nucleotide sequence in SEQ ID NO:1 encoding the mature form of the hPSP polypeptide having the amino acid sequence from about amino acid residue 1 to about amino acid residue 231 of SEQ ID NO:2 (claim 4); or complete nucleotide sequence of the cDNA clone contained in ATCC Deposit No 97811(claim 6), or nucleotide sequence encoding the hPSP polypeptide having the complete amino acid sequence except the N-terminal amino acid encoded by the cDNA clone contained in ATCC Deposit No 97811 (claim 7) or nucleotide sequence encoding the mature form of the hPSP (claim 8); (2) *any* isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95 % identical to a sequence selected from the group recited in claim 5; (3) an isolated nucleic acid molecule comprising a nucleic acid sequence which encodes an epitope-bearing portion of an hPSP polypeptide selected from the group recited in claim 9; (4) a method of making *any* recombinant vector , (claims 10 and 31), *any* recombinant vector (claims 11 and 31), a method of making *any* recombinant host cell (claim 12) and a recombinant host cell (claims 13 and 33) and a method for producing a hPSP (claims 14 and 34); (5) *any* isolated nucleic acid molecule comprising a polynucleotide having a sequence at least 95 % identical to a sequence selected from the group recited in claim 18; (6) *any* isolated polynucleotide comprising a nucleic acid sequence selected from the group recited in Claim 19, or comprising SEQ ID NO:1 (claim 22) or encoding a mature polypeptide (claim 24) or identical to the human cDNA contained in ATCC Deposit No. 97811 (claim 25) or encoding at least 50 contiguous amino acids of SEQ ID NO:2 (claim 27) or complementary to the polynucleotide of claim 19 (claim 28) ; (8) *any* isolated polynucleotide of claim 19, further comprising a hetorologus polynucleotide (claim 29), wherein said heterologous polynucleotide encodes a heterologous polypeptide (claim 30); (9) a composition comprising *any* isolated polynucleotide of claim 19 (claim 36)

Applicant has disclosed specific nucleic acid of SEQ ID NOS: I and amino acid of SEQ ID NO:2 therefore, the skilled artisan cannot envision all the contemplated nucleic acid sequence possibilities recited in the instant claims. Consequently, conception cannot be achieved until a representative description of the structural and functional properties of the claimed invention has occurred, regardless of the complexity or simplicity of the method. Adequate written description requires more than a mere statement that it is part of the invention. The sequence themselves are required. See *Fiers v. Revel*, 25 USPQ2d 1601, 1606 (CAFC1993). The Guidelines for the Examination of Patent Application Under the 35 U.S.C.112, 1"Written Description" Requirement make clear that the written description requirement for a claimed genus may be satisfied through sufficient description of a representative number of species disclosure of relevant, identifying characteristics, i.e., structure or other physical and or chemical properties, by functional characteristics coupled with a known or disclosed correlation between function and structure, or by a combination of such identifying characteristics, sufficient to show the applicant

was in possession of the genus (Federal Register, Vol. 66, No. 4, pages 1099-1111, Friday January 5, 20001, see especially page 1106 3rd column).
Vas-Cath Inc. v. Mahurkar, 19 USPQ2d 1111, makes clear that "applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession of the invention. The invention is, for purposes of the written description inquiry, whatever is now claimed." (See page 1117.) The specification does not "clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed." (See Vas-Cath at page 1116.). Consequently, Applicant was not in possession of the instant claimed invention. See University of California v. Eli Lilly and Co. 43 USPQ2d 1398.

Applicant is directed to the Revised Interim Guidelines for the Examination of Patent Applications Under the 35 U.S.C. 112, ¶ 1 "Written Description" Requirement, Federal Register, Vol. 66, No. 4, pages 1099-1111, Friday January 5, 2001.

12. The following is a quotation of the second paragraph of 35 U.S.C. 112.
The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

13. Claims 1, 4-5, 9-14, 18-19, 28-34 and 36 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

A). Claims 1 and 5 recites "having a nucleotide sequence at least 95% identical" and claim 18 recites "a polynucleotide having a sequence at least 95% identical". Percent sequence identity is not defined in the claim nor does it appear to be defined in the disclosure. Claim 19 recites " at least 95 % identical using Bestfit algorithm and default parameters". The characteristics and metes and bounds of this "default parameters" are unclear. The rejection can be obviated if Applicant can point to an explanation, in the disclosure, of how the identity calculation was made. This requires an algorithm and the parameters (e.g. gap penalties, mismatch penalties) to set.

B). Claim 4 recites "from about amino acid residue 1 to about 231 of SEQ ID NO: 2"; claim 5(d) recites " exclude from about 1 to about 43 amino acids from amino terminus"; claim 5(e) recites " excludes or from 1 to about 11 amino acid from carboxy terminus"; claim 9 recites "from about Ser 50 to about Leu 66 of SEQ ID NO:2" or "from about Glu 97 to about Leu 105 of SEQ ID NO:2" or "from about Glu 141 to about Gln 148 of SEQ ID NO:2"or "from about Asp 219 to about Leu 227 of SEQ ID NO:2" It is unclear how many amino acids constitute "about". One of skill in the art would not know if applicant meant one or two or several amino acids. In addition, the phrase "from about" in Claim 9, 3d line should not be used twice.

C). Claim 5(a) recites "at position n-231 in SEQ ID NO:2 ; Claim 5(b) recites "1-m of SEQ ID NO:2"; Claim 5 (c) recites "n-m of SEQ ID NO:2". It is unclear what Applicant means by "n-231" or "1-m" or "n-m"?

D). Claim 14 recites " a recombinant method for producing a hPSP". It is unclear what Applicant means by "recombinant method"?

E). Claim 19 recites "sequence selected fragment from the group". Ii is unclear what Applicant means by "fragment from the group"?

14. The nucleic acid of SEQ ID NOs: 1 is free of prior art.

15. No Claims are allowed.

16. The lengthy specification has not been checked to the extent necessary to determine the presence of all possible minor errors. Applicant's cooperation is requested in correcting any errors of which Applicant may become aware in the specification.

17. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Michail Belyavskyi whose telephone number is (703) 308-4232. The examiner can normally be reached Monday through Friday from 9:00 AM to 5:30 PM. A message may be left on the examiner's voice mail service. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Christina Chan can be reached on (703) 308-3973. Any inquiry of a general nature or relating to the status of this application should be directed to the Technology Center 1600 receptionist whose telephone number is (703) 308-0196.

Papers related to this application may be submitted to Technology Center 1600 by facsimile transmission. Papers should be faxed to Technology Center 1600 via the PTO Fax Center located in Crystal Mall 1. The faxing of such papers must conform with the notice published in the Official Gazette, 1096 OG 30 (November 15, 1989). The CM1 Fax Center telephone number is (703) 305-3014.

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October 21, 2002

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